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(57) Abstract

This invention provides recombinant DNA molecules which code for polypeptides that exhibit the antigenicity of an Aln g I allergen of alder, Alnus sp., of a Cor a I allergen of hazel or of a Bet v I allergen of birch and other plants of the order Fagales, and for polypeptides comprising at least one epitope thereof, as well as nucleic acids which under stringent conditions hybridize with such DNA sequences or are derivable from such sequences by degeneracy of the genetic code. In addition, methods are described for using the polypeptides coded by these DNA molecules and their use in the diagnosis or therapy of allergic diseases.

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ALLERGENS OF ALDER POLLEN AND APPLICATIONS THEREOF

1. FIELD OF THE INVENTION

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The invention provides recombinant DNA molecules which code for polypeptides, and the polypeptides per se, that have at least one epitope of an Aln g I pollen allergen, or a Cor a I pollen allergen or a Bet v I pollen allergen of a tree of the order Fagales, particularly alder, Alnus sp., or the entire Aln g I allergen protein, particu10 larly hazel, Corylus sp., or the entire Cor a I allergen protein, or particularly birch, Betula sp., or the entire Bet v I allergen protein, and exhibit the same or similar antigenicity as the Aln g I, the Cor a I or the Bet v I allergen. The invention also provides replicable microbial expression vehicles and microorganisms for use in processes for producing such allergenic polypeptides. Methods are provided for the diagnosis and therapy of allergic diseases using the synthetic polypeptides of the invention.

2. BACKGROUND OF THE INVENTION

It has long been known that a type I allergy to pollen proteins is associated with 20 symptoms such as itchy and reddened eyes, running nose, swollen eyelids, coughing and asthmatic conditions. In this respect, the pollens of early-flowering trees of the order Fagales (e.g., birch, hazel, alder and hornbeam) hold an important position. Numerous studies have been carried out to identify and characterize the allergens of these pollens precisely (1 - 4). Progress with regard to the exact characterization of 25 pollen allergens has been hindered by the heterogeneity of the pollen extracts currently in use. Some eight allergens of alder pollen elicit an IgE response in atopics and one of them, Aln g I, a 17 kD protein, reacts with a majority of the sera of allergic patients as the major allergen (5, 6).

At least 10 % of the population suffers from pollen allergies at various times 30 and to varying extent. These allergies are mediated by IgE antibodies which react

with pollen proteins. The possibility exists for a therapy for pollen allergies by hyposensitization, i.e., by the regular and slowly increasing administration of the proteins producing the allergy.

Diagnostic methods for allergic diseases, such as radio-allergosorbent test 5 (RAST), paper radioimmunosorbent test (PRIST), enzyme-linked immunosorbent assay (ELISA), radioimmunoassays (RIA), immuno-radiometric assays (IRMA), luminescence immunoassays (LIA), histamine release assays, and IgE immunoblots depend greatly upon the availability of pure allergens. Protein extracts from pollen isolated from natural sources are difficult to standardize because preparations vary 10 from batch to batch. For example, they may contain unwanted constituents, and/or certain proteins may be lost in the extraction procedure and be missing from the final preparation (7). Clearly, diagnostic tests which employ well defined allergens that can be reproducibly prepared would be superior to tests which employ raw pollen extracts with an insufficiently defined mixture of allergens and other components.

15 Recombinant DNA production of allergenic polypeptides, or allergenic fragments thereof, would allow more reproducible preparations of allergens of defined content for standardized diagnostic and therapeutic methods.

Allergens may be purified to homogenity from pollen by known protein/chemical methods, for example, by means of affinity chromatography (8). These methods 20 are relatively costly and require pollen as an expensive source for allergens. It would, therefor, be cheaper and more efficient to use recombinant DNA methods to produce an allergenic protein, or fragments of that protein.

Hyposensitization has proved to be an effective therapy in allergic diseases.

This therapy consists of parenteral or oral administration of allergens in increasing

25 doses over a fairly long period of time.

ic says

3. SUMMARY OF THE INVENTION

The present invention provides recombinant DNA molecules which contain a nucleotide sequence that codes for a polypeptide which exhibits the same or similar 5 antigenic properties as the major allergen, Aln g I, Cor a I or Bet v I of trees of the order Fagales, for example, of alder (Alnus sp.), hazel (Corvlus sp.) or birch (Betula sp.) or a polypeptide which comprises at least one epitope of such allergens. The invention provides the complete cDNA sequence of an Alng I, a Cor a I or a Bet v I allergen and hence the complete deduced amino acid sequences. Additionally, the 10 invention includes (a) nucleotide sequences which hybridize with such a cDNA sequence under high stringency and encode a polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen and (b) nucleotide sequences which can be derived from such allergenic polypeptides by degeneracy of the genetic code. This nucleotide sequence can be expressed as an Alng I. a Cor a I or a Bet v I allergen, or 15 as a polypeptide which comprises at least one epitope thereof. In a preferred embodiment, this cDNA sequence contains the whole sequence or parts of the sequence set forth in the Sequence Listing as SEQ ID NO. 2 for Alng I, as SEQ.ID NO.10, 13, 16 and 19 for Cor a I and as SEQ ID NO. 22 for Bet v I.

As concerns their IgE binding, pollens of birch, alder, hazel and hornbeam 20 possess similar major allergens which - so far as is known - exhibit a high degree of homology on the amino acid level. The present invention therefore relates not only to an Aln g I allergen of alder, or Cor a I of hazel or Bet v I of birch, but as well to Aln g I. Cor a I or Bet v I pollen allergens of other species which are coded by DNA allergen under stringent conditions or can be derived from such polypeptide allergens 25 by degeneracy of the genetic code.

Hybridization of a polynucleotide with another polynucleotide under stringent conditions requires at least a 60 % identity between such polynucleotides at the nucleic acid level.

Such stringent conditions entail washing of hybridized nitrocellulose filters as 30 follows:

- (a) For DNA/DNA and DNA/RNA hybridizations: A temperature of 55°C, a salt concentration of 150 mM NaCl and 15 mM Na₃ citrate at pH 7,0, and a SDS (Sodium Dodecyl Sulfate) detergent at a concentration of 0,1 % (w/v).
- (b) For oligodeoxynucleotide/DNA hybridizations: A temperature of 55°C, a 5 salt concentration of 1M NaCl and 10 mM Na₃citrate x 2H₂O at pH 7,0, and a SDS (Sodium Dodecyl Sulfate) detergent at a concentration of 0,5 % (w/v). In this context "oligodeoxynucleotide" refers to an oligomer of a single-stranded DNA of up to 100 nucleotides in length.

In addition, this invention provides expression plasmids that contain a nucleoti10 de sequence as described above and host cells which harbor these expression plasmids.

This invention also provides compositions containing synthetic polypeptides which exhibit the antigenicity of parts or of the whole of an alder Aln g I allergen or of allergens of other plants which, because of a high degree (at least 50 %) of amino 15 acid homology (9), exhibit antigenic cross-reactivity to parts or to all of an alder Aln g I allergen, i.e., antibodies or cellular antigen binding sites which are actually directed to alder Aln g I allergen are likewise able to bind to these molecules. These synthetic polypeptides include fusion and nonfusion polypeptides which contain a polypeptide portion that possesses the antigenicity of a part or of all of an alder poly-20 peptid which contain a polypeptide portion that possesses the antigenicity of a part or of all of an Aln g I, a Cor a I or a Bet v I allergen. The method for preparing such synthetic polypeptides comprises the steps of culturing of prokaryotic or eukaryotic host cells which contain an expression plasmid described above and purification of the synthetic polypeptide(s) from the culture.

The term "synthetic" here alternatively includes polypeptides which are prepared by cloning and expression of the nucleotide sequences described here or by chemical synthesis of polypeptides encoded by these nucleotide sequences.

The synthetic polypeptides which are produced according to this invention exhibit antigenicity the same as or similar to the native allergen. As shown below, a 30 cDNA clone coding for an alder Aln g I, a hazel Cor a I or a birch Bet v I can be

used to produce a nonfusion polypeptide which reacts with IgE in the sera of allergic persons. It is therefore possible to use this polypeptide as an antigen in diagnostic tests (such as RAST, PRIST, ELISA, RIA, IRMA, LIA, histamine release assays and IgE immunoblots known in the art and referred to above), as a component of prophy-5 lactic or therapeutic agents in hyposensitization therapy, and as a component in any kind of in vivo diagnostic procedure such as bronchial, conjunctival, dermal, nasal and oral provocation and skin tests.

In particular, the synthetic allergens can be used as diagnostic reagents in vitro and in vivo, since their antigenicity corresponds to that of the native Aln g I pollen 10 allergens and they are therefore able to bind IgE of sera of persons suffering from Aln g I pollen allergy. In the same way, the antigenicity corresponds to that of the native Cor a I or Bet v I pollen allergens and they are also able to bind IgE of sera of sensitive or allergic patients.

It is therefore one of the objects of the present invention to provide a method 15 for the preparation of pollen allergens, in particular for Aln g I. Cor a I or Bet v I allergens, so as to have this family of allergens available for diagnostic tests for detection of the corresponding allergy and, alternatively, for hyposensitization therapy.

As main epitopes capable of modifying T-cell response the following amino acid sequences were found:

- 20 GlyValPheAsnTyrGlu
 PheIleLeuAspGlyAspLysLeu
 AlaIleSerSerValGluAsnIle
 GlyAsnGlyGlyProGlyThrIleLysLysIleSerPhe
 LysTyrValLysAspArgValAspGluValAsp
- 25 LeuLeuArgAlaValGluSerTyrLeuLeuAlaHisSer.

 All these sequences are present in all said allergens, i.e. Aln g I, Cor a I and

 Bet v I.

4. BRIEF DESCRIPTION OF THE FIGURES

The following figures and description aid in understanding the field and scope 5 of the invention.

- FIG. 1 shows a cDNA (665 nucleotides, SEQ ID NO.1) encompassing the nucleotide sequence encoding an Aln g I allergen of alder. The cDNA sequence consists of a coding region of 483 nucleotides (including the initation and termination codons), a 3' noncoding region of 162 nucleotides and a poly-A tail of 20 nucleotides.
- 10 The deduced amino acid sequence of alder Aln g I polypeptide is indicated in FIG. 1 under the respective codons. The complete protein has 160 (SEQ ID NO.3) amino acids (including the methionine of the initiation codon).
- FIG. 2 shows the nucleotide sequence of the BP-A primer (SEQ ID NO.4) that was used for synthesis of the first cDNA strand. The recognition sequences of the 15 restriction enzymes BgIII (nucleotides 19-24) and HindIII (nucleotides 31-36) are underlined. The sequence of T7 primer (nucleotides 4-17), which was used as primer for the PCR amplification of Aln g I and is the constituent of BPA, is likewise indicated.
 - FIGS. 3 10 show Immunoblot analysis of isoforms of the major hazel pollen allergen Cor a I as recombinant non-fusion proteins, in particular
- 20 FIGS. 3 6:

An identical set of patients' sera was used to characterize the <u>Cor a I</u> isoforms (lanes 1 - 9).

Lanes B: buffer control without addition of patients' sera.

Lanes N: a pool of non-allergic normal human sera.

IgE antibodies from the allergic patients' sera, which bound to the isoforms, was detected by ¹²⁵I labeled rabbit-anti human IgE. Each of the isoforms shows reactivity with IgE from allergic patients' sera. All isoforms were able to bind IgE, although their individual binding pattern may differ from patient to patient.

FIG. 7:

An identical set of experiments was performed using E.coli JM 105 transformed with the plasmid pKK 223.3 without any cDNA insertion. No bound IgE could be 5 detected.

FIG. 8:

Likewise the cDNA fragment whose sequence is shown in SEQ ID NO. 1 was ligated into the expression plasmid pKK 223.3. The protein corresponding to the coding region (see SEQ ID NO. 2 and SEQ ID NO.3) was expressed in E.coli JM 10 105 and tested with the identical set of patients' sera as above. rAln g I was able to bind IgE from these patients' sera in each case (lanes 1 - 9). In lanes B (buffer control, no patients' sera) and N (a pool of sera from non allergic individuals) no binding could be observed.

FIG. 9:

This represents the quality control of the patients' sera used in the above experiments. The very same set of sera was tested on separated and blotted proteins from an aqueous extract of birch pollen. IgE from every single serum bound strongly to the major allergen of birch pollen, <u>Bet v I</u> (lanes 1 - 9). No binding could be observed for the buffer control (lane B) and the pool of sera from non allergic individuals.

20 FIG.10:

Furthermore the same sera were tested on rBet v I and showed exactly the same strong reactivity with the recombinant nonfusion protein.

FIG. 11:

Inhibition experiment showing the capacity of <u>rBet v I</u> to bind IgE from tree 25 pollen allergic patients' sera and thus to prevent the IgE from further binding to the corresponding hazel pollen allergen <u>Cor a I.</u> 1 ml each of a 1: 10 dilution of birch pollen allergic individuals' sera (1 - 5), of a serum pool of non allergic individuals (6), and buffer without the addition of serum (7) was incubated over night at 4°C with the addition of 5 µg of <u>rBet v I</u> (panel 1), 5 µg of BSA (panel 2), or buffer only 30 (panel 3). These samples were used to probe a Western blot of SDS-PAGE-separated

hazel pollen proteins. In the case where <u>rBet v I</u> had been added no IgE binding to the 17kD <u>Cor a I</u> could be observed. The addition of bovine serum albumin (BSA) or buffer without addition of a protein could not inhibit the binding of patients' IgE to the hazel <u>Cor a I</u>.

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5. EXAMPLES

- 5.1. Poly A+ RNA isolation from pollen and synthesis of the first cDNA strand:
- Polyadenylated (polyA+) mRNA was isolated from ripe alder pollen (Allergon AB, Engelsholm, Sweden) (l). Using this, the first strand of cDNA was synthesized as follows:
 - 2 µl 10x buffer (480 mM Tris (hydroxymethyl) aminomethane (Tris), 60 mM MgCl₂, 400 mM KCl, pH 4,8)
- 15 2 μl 10 mM dithiothreitol (DTT)
 - 1 µl primer BP-A (100 ng/µl, nucleotide sequence of FIG.2) (SEQ ID NO.4)
 - 2 μl 25 mM deoxynucleoside triphosphates (dNTPs), i.e. 25 mM each of dATP, dCTP, dGTP, dTTP (Pharmacia, Uppsala, Sweden)

11 µl H₂O

20 1 µl poly A+RNA (3 µg)

1 μ l AMV reverse transcriptase (United States Biochemical Corporation (USB), Cleveland, Ohio, USA) = 32 Units.

This reaction, with a total volume of 20 µl, was incubated for 2 hours at 42°C, then diluted 1:1 with 1x TE buffer (10 mM Tris, 1mM ethylenediamine tetraacetic 25 acid (EDTA), pH 8,0) and stored at 4°C.

5.2 Polymerase chain reaction (PCR):

PCR was carried out on the hybrid RNA-DNA molecules prepared in Section 5.1. A mixture of the following two oligodeoxynucleotides was used as primer for the 5'-end of the molecules:

No. 2482 (SEQ ID NO.5)

5'- GTT TTC AAT TAC GAA GCG GAA AC -3'

No.2490 (SEQ ID NO.6)

5'- GTT TTC AAT TAC GAA GCG GAG AC -3'

The nucleotide sequences of these oligodeoxynucleotides were derived from the N-terminal amino acid sequence of alder Aln g I partially determined by Edman degradation and following the codon usage of birch (B. verrucosa).

T7 primer (SEQ ID NO.7) (Pharmmacia), which is likewise a constituent of the BP-A primer, was used as primer for the 3' end of the molecules. The following 10 mixture was used for the reaction:

- 2,5 µl of the reaction mixture in Section 5.1
- $5.0 \mu 1.10 \text{x}$ PCR buffer (400 mM KCl, 10 mM MgCl₂, 10 % gelatin, 100 mM Tris, pH 8.3)
 - 2,0 µl T7 primer (SEQ ID NO.7) (Pharmacia) = 20 pmol
- 4,0 μ l primer mix in equal parts of No. 2482 (SEQ ID NO.5) and 2490 (SEQ ID NO.6) = 100 pmol
 - 2,5 µl 2 mM dNTPs (Pharmacia)
 - 1,5 山 100 mM MgCl₂
 - 32,5 μ l H₂O (to 50 μ l)
- Addition of 1 unit Taq DNA polymerase (USB). The reaction mixture was incubated for 30 seconds at 93°C, for 30 seconds at 55°C and for 1 minute at 72°C. This cycle was run through 30x in all. Finally, the reaction mixture was kept at 72°C for another 10 minutes.
 - 5.3 Cloning of the PCR fragment and sequencing:
- The DNA fragment synthesized in Section 5.2 was isolated from a 1,5 % agarose gel by means of DEAE paper (10). This fragment was then kinased at the 5'-end.
 - a) Kinasing
 - 10 Д DNA (= 500 ng <u>Aln g I</u> DNA)
- 30 2,5 µl 10x T4 polynucleotide kinase buffer (Boehringer, Mannheim, Germany)

7,0 µl γ-32P-ATP, 10 mCi/ml (Amersham, Little Chalfont, England

4.5 µ1 H₂O

1,0 µl polynucleotide kinase (Boehringer)

The reaction mixture was incubated for 20 minutes at 37°C. After that another 5 addition of 1 μ l polynucleotide kinase was made and the mixture was incubated for 60 minutes at 37°C.

b) Klenow fill-in reaction:

To the above reaction mixture was added:

1 μl 2mM dNTPS (Pharmacia)

10 1 μ l Klenow Fragment (= 2 units)

The kinased and filled-in DNA fragment was purified by way of a NickTM Column (Pharmacia) and was then precipitated with ethanol and sodium acetate (9).

c) BglII digestion of fragment:

Several restriction enzyme sites were added at the 3'-end to the Aln g I sequen15 ce through the use of the BP-A oligodeoxynucleotide (FIG.2; SEQ ID NO.4) in the
PCR. The BgIII site in this sequence was selected for cleavage with the restriction
enzyme, BgIII, to ligate the fragment in the corresponding BgIII site of pBluescript^R
plasmid (Stratagene, LaJolla, California, USA). Due to the Klenow reaction, blut
ends had already been produced at the 5'-end of the sequence. All the DNA precipita-

- 20 ted in Section 5.3b was dissolved in 2 μ l 10x BglII buffer (Boehringer). 17 μ l H₂O and 1 μ l BglII (Il units) were added. The reaction mixture was incubated for 1,5 hours at 37°C. The fragment so cut was eluted from a 1,5% agarose gel by means of DEAE paper (10).
 - d) Ligation of the DNA fragment in pBluescript-R KS+ plasmid:
- pBluescript^R KS+ plasmid (Stratagene) was selected as cloning vector and cut with the restriction enzymes EcoRV (supplies flush ends; the 5'-end of the Aln g I fragment is ligated to these) and BamHI (supplies staggered ends compatible with BglII; the 3'-end of the Aln g I fragment is ligated to these). The phosphate groups at the 5'-ends of the plasmid were removed by alkaline phosphatase (12) to prevent non-30 specific religation of the vector.

Ligation of Aln g I fragment in pBluescript^R KS+ plasmid:

20 ng DNA from Section 5.3c dissolved in 10 μ H₂O

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- 2,0 µl 10x ligation buffer (200 mM Tris, 50 mM MgCl₂, 50 mM DTT, 500 µg/ml bovine serum albumin; pH 7,6)
- 5 1,0 μl 10 mM ATP
 - 3,0 µl pBluescript^R KS+ cut with EcoRV and BamHI (= 50 ng)
 - 4,0 µl H₂O
 - 1,0 μ l T4 DNA ligase Boehringer (= 3 units)

This reaction was incubated for 4 hours at room temperature.

e) Transformation of competent <u>E.coli</u> host cells:

Transformation was carried out in <u>E.coli</u> XL1-Blue cells (Stratagene) (13). The selection of positive clones was carried out on ampicillin-containing (100 μ g/ml) culture plates by means of the blue-white indication system (14).

- f) Sequencing of Aln g I DNA:
- Sequencing of Aln g I DNA was carried out by means of a T7 sequencing kit (Pharmacia), according to the manufacturer's instructions.
 - 5.4 Expression of Aln g I DNA and detection of IgE binding of the resulting proteins:
- a) The DNA insert from the pBluescript^R KS+ vector, which contains the coding sequence for Aln g I, was subjected to mutagenesis according to Kunkel et al (15). To complete the Aln g I sequence at the 5'-end and provide it with the ATG codon and an additional EcoRI site, the following oligodeoxynucleotide was synthesized (SEQ ID NO.8): 5'-CTT CGT AAT TGA AAA CAC CCA TGA ATT CCG
- 25 ATA CCG TCG A -3' and used for mutagenesis. This enabled the Aln g I sequence to be ligated, in the correct orientation, by means of the EcoRI site at the 5'-end and by means of the HindIII site at the 3'-end of the gene in the expression plasmid pKK 223-3 (Pharmacia). E.coli Kl2 JMl05 cells (thi, rpsL, endA, sbcBl5, hsdR4, delta (lacpro AB)/F', thraD36, proAB, lacI4Z delta Ml5) were transformed with this plasmid. After protein synthesis was effected, the bacterial cells were harvested and bro-

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ken up with liquid nitrogen. The lysate was separated n a SDS polyacrylamide gel. Detection of recombinant Aln g I nonfusion protein was done by means of immunoblot. IgE in the sera of allergic patients was bound by the recombinant Aln g I. Detection of bound IgE was effected by ¹²⁵I-labeled antihuman IgE (Pharmacia).

b) The DNA insert in pBluescript^R KS+ plasmid, which contains the sequence coding for Aln g I, was ligated by means of EcoRI linkers (Boehringer) in the expression plasmids pEX A, pEX B and pEX C (16), which shift the reading frame of the insert one nucleotide each time. In this way, in one case the correct reading frame for Aln g I was obtained and the production of a recombinant Aln g I fusion protein was 10 induced. The capability of this recombinant Aln g I fusion protein to bind IgE in sera of patients allergic to alder pollen was shown by means of immunoblot. Detection of bound IgE was effected by ¹²⁵I-labeled antihuman IgE (Pharmacia).

An analogous method was applied for the cloning and expressing of Cor a I.

5.5 Expression of Cor a I DNA and detection of IgE binding of the resulting protein

The cDNA fragments whose sequences are shown in SEQ ID NO.9, 12, 15 and 18 were ligated into the expression plasmid pKK 223.3 (Pharmacia LKB Biotechnology, Uppsala, Sweden). The proteins corresponding to the coding region (see SEQ ID 20 NO.10, 13, 16 and 19) of these fragments were expressed in E.coli JM 105 transformed with the respective recombinant plasmids. Cultures were grown until the OD₆₀₀ reached 0,4. Isopropyl-β-D-galactopyranoside was then added to a final concentration of 0,5 mM and the cultures grown at 37°C over 3,5 hours for expression of recombinant non-fusion proteins. Bacterial cells were harvested by centrifugation, taken up in 25 50 mM Tris-HCl buffer, pH 7,5, containing 220 mM NaCl and the cells were disrupted by a freezethaw cycle. The supernatant containing the recombinant non-fusion proteins was loaded onto a 15 % SDS-PAGE. The separated proteins were transferred to a nitrocellulose filter. IgE-binding proteins were detected by the use of allergic patients' sera.

The results are shown in FIGS. 3 - 6.

5.6 Test of reaction of T-cell epitopes

Peripheral blood was collected from birch pollen allergic patients who showed igE reactivity to <u>Bet v I</u> exclusively, as demonstrated by Western Blot. Peripheral mononuclear cells (PBMC; the white blood cell fraction containing the lymphocytes) 5 were isolated by density gradient centrifucation. Allergen specific T-cells were enriched by culturing PBMC in presence of <u>Bet v I</u>. After a cloning procedure, T-cell clones (TCC) were proved to react with the complete <u>Bet v I</u> molecule by a proliferation assay, showing that in presence of the specific allergen a proliferation occurs, which is at least 10-fold higher than the autoproliferative activity of the TCC, as 10 measured by ³H-Thymidine incorporation. Two <u>Bet v I</u> specific TCC isolated from atopic donors reacted in the same way with the above mentioned peptides as with the whole <u>Bet v I</u> molecule, proving that these peptides represent or contain the relevant T-cell epitopes.

15

TCC	TCC+FC	TCC+FC+Bet v I	TCC+FC+PEPTIDE	
443	960	30516	31580*	cpm
160	508	21218	23309**	cpm

20 FC: feeder cells

cpm: counts per minute

* peptide: LLRAVESYLLAHS

**peptide: KYVKDRVDEVD

25 6. <u>METHODS OF ADMINISTRATION</u>

The present invention covers the use of the recombinant or synthetic polypeptide allergens to treat a mammal using such polypeptides alone or in combination with any pharmaceutically acceptable carriers or diluents, in accordance with standard pharmaceutical practice. The method of treatment involves the administration of such a polypeptide allergen or parts thereof by any route of administration, that is bronchial, conjunctival, dermal, enteral, nasal, oral or vaginal. A range of from 1 picogram to 10 milligrams per application can be used. The diluents and carriers can be chosen by those skilled 5 in the art according to commonly accepted galenic procedures. Like diagnostic methods, it requires pure and well defined allergens. The use of purified recombinant allergens or synthetic peptides would greatly reduce the risk of sensitizing patients to unwanted components.

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SEQUENCE LISTING

(i) APPLICANT:

Dr. Heimo Breiteneder

Mag. Arnold Reikerstorfer

Dr. Rudolf Valenta

Mrs. Dr. Karin Hoffmann -

Sommergruber

Dr. Michael Breitenbach

Dr. Dietrich Kraft

Dr. Helmut Rumpold

Dr. Otto Scheiner

(ii) TITLE OF INVENTION: ALLERGENS OF ALDER POLLEN
AND APPLICATIONS THEREOF

(iii) NUMBER OF SEQUENCES: 23

15 (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Pennie & Edmonds
- (B) STREET: 1155 Avenue of the Americas
- (C) CITY: New York
- (D) STATE: New York
- 20 (E) COUNTRY: USA
 - (F) ZIP: 10036
 - (V) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
- 25 (C) OPERATING SYSTEM: MS-DOS
 - (D) SOFTWARE: WordPerfect 5.1
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/683,831
 - (B) FILING DATE: 11-APR-91
- 30 (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Harry C. Jones, III
 - (B) REGISTRATION NUMBER: 20,280
 - (C) REFERENCE/DOCKET NUMBER: 6530-009
- 35 (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-9741/8864

(2) INFORMATION FOR SEQ ID NO: 1:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

665

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(ii)	MOLECULE	TYPE:	CDNA	of	mRNA
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- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Alder (Alnus sp.)

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AAAAA

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INFORMATION FOR SEQ ID NO: 2: (3) SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 480 nucleotides (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear MOLECULE TYPE: cDNA of mRNA (ii) (iii) HYPOTHETICAL: No ANTI-SENSE: No (iv) ORIGINAL SOURCE: (vi) (A) ORGANISM: Alder (Alnus sp.) SEQUENCE DESCRIPTION: SEQ ID NO: 2: (xi) ATGGGTGTTT TCAATTACGA AGCGGAAACC CCCTCCGTTA TCCCAGCGGC TCGGCTGTTC 60 ARGCCTTTA TCCTTGATGG CGATAAGCTC CTTCCAAAGG TTGCACCTGA AGCTGTTAGC 120 15 AGTGTTGAGA ACATTGAAGG AAATGGAGGG CCTGGAACCA TCAAGAAGAT CACCTTTCCC 180 GAAGGCAGCC CTTTTAAGTA CGTAAAGGAG AGGGTTGATG AGGTTGATCG CGTAAACTTC 240 ARATACAGCT TCAGCGTGAT CGAGGGTGGT GCCCTGGGCG ACGCACTGGA GAAGGTCTGT 300 AACGAGATCA AGATAGTGGC AGCCCCTGAT GGAGGATCCA TCTTGAAGAT CAGCAACAAG 360

20 GCCGTGGGAC TTCTCAAGGC CGTTGAGAGC TACCTCTTGG CACACTCTGA TGCCTACAAC 480

25

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Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Va 25 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As	
(B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: polypeptide (iii) HYPOTHETICAL: No (vi) ORIGINAL SOURCE: (A) ORGANISM: Alder (Alnus sp.) (xi) SEQUENCE DESCRIPTION: SEQ ID No: 3: Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Pro Ser Val II 1 5 10 15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20 25 3 Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Va 25 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 31 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140	
S (D) TOPOLOGY: linear (ii) MOLECULE TYPE: polypeptide (iii) HYPOTHETICAL: No (vi) ORIGINAL SOURCE: (A) ORGANISM: Alder (Alnus sp.) 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Pro Ser Val II 1 5 10 15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20 25 3 Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Val 25 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 31 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140	
(ii) MOLECULE TYPE: polypeptide (iii) HYPOTHETICAL: No (vi) ORIGINAL SOURCE: (A) ORGANISM: Alder (Alnus sp.) (xi) SEQUENCE DESCRIPTION: SEQ ID No: 3: Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Pro Ser Val II 1 5 10 15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20 25 3 Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Va 25 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 31 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
(iii) HYPOTHETICAL: No (vi) ORIGINAL SOURCE: (A) ORGANISM: Alder (Alnus sp.) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Pro Ser Val II 1 5 10 15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20 25 3 Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Va 25 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 31 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
(vi) ORIGINAL SOURCE:	
(A) ORGANISM: Alder (Alnus sp.) (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Pro Ser Val II 1 5 10 15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20 25 3 Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Va 25 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 31 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Pro Ser Val II 1 5 10 15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20 25 3 Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Val 25 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 315 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Pro Ser Val II 1 5 10 15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20 25 3 Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 61y Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Val Asp Arg Val Asp Glu Val Asp Arg Val Asp 65 75 65 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 60 60 11 Ser Ile Leu Lys Ile Ser Asn Lys Ile Val Ala Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 116 Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al 140	
1 5 10 15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20 25 3 Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Val 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 Tle Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
1 5 10 15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20 25 3 Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35 40 45 20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Val 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 Tle Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
15 AlaArg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Lys Leu 20	
Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35	15
Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35	vs Leu Leu Pro
Lys Val Ala Pro Glu Ala Val Ser Ser Val Glu Asn Ile Gl 35	30
20 Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Va 25 65 Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 116 Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gl 50	Ile Glu Gly Ası
Gly Gly Pro Gly Thr Ile Lys Lys Ile Thr Phe Pro Glu Gly 50	45
50 55 60 Phe Lys Tyr Val Lys Glu Arg Val Asp Glu Val Asp Arg Val 75 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
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25 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
25 65 70 75 Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
Lys Tyr Ser Phe Ser Val Ile Glu Gly Gly Ala Val Gly As 85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Val 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	Arg Val Asn Phe
85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	80
85 90 30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	-1 1 -
30 Glu Lys Val Cys Asn Glu Ile Lys Ile Val Ala Ala Pro As 100 105 11 Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	_
Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	95
Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	Pro Asn Clu Clu
Ser Ile Leu Lys Ile Ser Asn Lys Phe His Thr Lys Gly As 115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	110
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115 120 125 35 Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	Gly Asp His Glu
Ile Asn Ala Glu Gln Ile Lys Ile Glu Lys Glu Lys Ala Va 130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
130 135 140 Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	
Leu Lys Ala Val Glu Ser Tyr Leu Leu Ala His Ser Asp Al	Ala Val Gly Lev
	_
40 145	Asp Ala Tyr Asr

	(2)	INCOMMITON TOWN DOE	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 50 nucleotides	
		(B) TYPE: nucleic acid	
5		(C) STRANDEDNESS: single	
_		(D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: Other nucleic acid-synthetic	
		(iii) HYPOTHETICAL: Yes	
	•	(ix) FEATURE:	
10		(D) OTHER INFORMATION: Primer for reverse	
		transcription	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
		· ·	
	TTTA	ATACGA CTCACTATAG ATCTCCCGGG AAGCTTTTTT TTTTTTTTTT	50
15			
	(6·)		
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 23 nucleotides	
		(B) TYPE: nucleic acid	
20)	(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: Other nucleic acid-synthetic	
		(iii) HYPOTHETICAL: Yes	
		(vi) ORIGINAL SOURCE:	
25	5	(C) INDIVIDUAL/ISOLATE: 2482	
		(ix) FEATURE:	
		(D) OTHER INFORMATION: Primer for	
		polymerase chain reaction (PCR)	
		utilized at the 5' end of Aln g I mRNA	
30	0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
		GTTTCAATT ACGAAGCGGA AAC 23	

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	(7)	INFORMATION FOR SEQ ID NO: 6:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 23 nucleotides	
		(B) TYPE: nucleic acid	
5		(C) STRANDEDNESS: single	,
		(D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: Other nucleic acid-synthet	ic
		(iii) HYPOTHETICAL: Yes	
		(vi) ORIGINAL SOURCE:	
10		(C) INDIVIDUAL ISOLATE: 2490	
		(ix) FEATURE:	
		(D) OTHER INFORMATION: Primer for	
		polymerase chain reaction utilized a	ıt
		the 5' end of Aln g I mRNA	
15		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
		GTTTTCAATT ACGAAGCGGA GAC 23	
	(8)	INFORMATION FOR SEQ ID NO: 7:	
		(i) SEQUENCE CHARACTERISTICS:	
20		(A) LENGTH: 14 nucleotides	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: Other nucleic acid-synthet	ic:
25		(iii) HYPOTHETICAL: Yes	
		(ix) FEATURE:	
		(D) OTHER INFORMATION: Primer for	
		polymerase chain reaction (PCR)	
		utilized at the 3' end of Aln g I m	ANS
30		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
		ARTACGACTC ACTA > 14	
	(9)	INFORMATION FOR SEQ ID NO: 8:	
		(i) SEQUENCE CHARACTERISTICS:	
35		(A) LENGTH: 40 nucleotides	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: Other nucleic acid-synthet	ic:
40		(iii) HYPOTHETICAL: Yes	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
		CTTCGTARTT GARACACCC ATGARTTCCG ATACCGTCGA	40

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INFORMATION FOR SEQ ID NO: 9

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 619 nucleotides

 (B) TYPE: nucleic acid

 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA of mRNA
- (iii) HYPOTHETICAL: no
- 10 (iv) ANTI-SENSE: no
 - (V) FRAGMENT TYPE: not applicable
 - (vi) ORIGINAL SOURCE:
 (A) ORGANISM: hazel (Corylus sp.)
 - (vii) IMMEDIATE SOURCE:
- 15 (A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
 - (viii) POSITION IN GENOME: not applicable
 - (ix) FEATURE: not applicable
 - (*) PUBLICATION INFORMATION: not applicable
- 20 (xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 9

	ATGGGTGTTT	TCAATTACGA	GGTTGAGACT	CCCTCCGTTA	TCCCTGCGGC	50
	AAGGCTGTTC					100
			AGCGTTGAAA			150
25			CACCTTTGGC			200
			AGGTTGACAA			250
			GTCCTGGGTG			300
			AGCCCCTGGT			35.0
			AAGGCGACCA			400
30			GCAGAGAAAC			450
-			TGAATACAAC			500
			GTGGCTTTCA			550
			GCTTGCGGTT			600
	GILIACITOC					619

	(1)	SEQUENCE CHARACTERISTICS.	
		(A) LENGTH: 480 nucleotides	
5		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA of mRNA	
	(iii)	HYPOTHETICAL: no	
10	(iv)	ANTI-SENSE: no	
	(v)	FRAGMENT TYPE: not applicable	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: hazel (Corylus sp.)	
	(vii)	IMMEDIATE SOURCE:	
15		(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN	
	(viii)	POSITION IN GENOME: not applicable	
	(ix)	FEATURE: not applicable	
	(x)	PUBLICATION INFORMATION: not applicable	
20	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO: 10	
		GTTT TCAATTACGA GGTTGAGACT CCCTCCGTTA TCCCTGCGGC	50
		GTTC ARGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG	100
		CTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG	
25		ACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA	
		GGAG AGGGTTGATG AGGTTGACAA CACAAACTTC ACATACAGCT	250
		TGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC	300
	-	CTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT	
		CARG TTCCACGCCA AAGGCGACCA TGAGATTAAT GCAGAGGAGA	400
30	TGAAGG	GTGC CAAAGAAATG GCAGAGAAAC TTTTAAGGGC GGTTGAGACC	450
	TACCTA	TTGG CACACTCTGC TGAATACAAC	480

- (i) SEQUENCE CHARACTERISTICS: Cor a I 5 (c)
 - (A) LENGTH: 160 amino acids
- 5 (B) TYPE: amino acid
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: not applicable
- 10 (V) FRAGMENT TYPE: not applicable
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: hazel (Corylus sp.)
 - (vii) IMMEDIATE SOURCE:
 - (A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
- 15 (viii) POSITION IN GENOME: not applicable
 - (ix) FEATURE: not applicable
 - (x) PUBLICATION INFORMATION: not applicable
 - (xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 11

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- 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 Met Gly Val Phe Asn Tyr Glu Val Glu Thr Pro Ser Val Ile Pro
- 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 25 Ala Ala Arg Leu Phe Lys Ser Tyr Val Leu Asp Gly Asp Lys Leu
 - 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 Ile Pro Lys Val Ala Pro Gln Ala Ile Thr Ser Val Glu Asn Val
- 30 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 Glu Gly Asn Gly Gly Pro Gly Thr Ile Lys Asn Ile Thr Phe Gly
- 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 Glu Gly Ser Arg Tyr Lys Tyr Val Lys Glu Arg Val Asp Glu Val
 - 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 Asp Asn Thr Asn Phe Thr Tyr Ser Tyr Thr Val Ile Glu Gly Asp
- 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 40 Val Leu Gly Asp Lys Leu Glu Lys Val Cys His Glu Leu Lys Il
 - 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 Val Ala Ala Pro Gly Gly Gly Ser Ile Leu Lys Ile Ser Ser Lys

121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 Phe His Ala Lys Gly Asp His Glu Ile Asn Ala Glu Glu Met Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 5 Gly Ala Lys Glu Met Ala Glu Lys Leu Leu Arg Ala Val Glu Thr

151 152 153 154 155 156 157 158 159 160 Tyr Leu Leu Ala His Ser Ala Glu Tyr Asn

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	(i)	SEQUENCE CHARACTERISTICS:	
	•	(A) LENGTH: 742 nucleotides	
5	•	(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: Bingle	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA of mRNA	
	-	HYPOTHETICAL: no	
10	(iv)	ANTI-SENSE: no	
		FRAGMENT TYPE: not applicable	•
		ORIGINAL SOURCE:	
	•	(A) ORGANISM: hazel (Corylus sp.)	
	(vii)	IMMEDIATE SOURCE:	
15	•	(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN	
	(viii)	POSITION IN GENOME: not applicable	
	-(ix)	FEATURE: not applicable	
	(x)	PUBLICATION INFORMATION: not applicable	
20	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO: 12	
		·	50
	ATGGGT	GTTT TCAATTACGA GGTTGAGACT CCCTCCGTTA TCCCAGCGGC	
	AAGGCI	CETTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG	150
	TTGCAC	CCTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG	
25	CCTGG	ARCCA TCARGARTAT CACCTTTGGC GARGGCAGCC GTTACAAGTA	200 250
	CGTGAF	AGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC AAATATAGCT	300
	ACACCO	STGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTCGGA GAAGGTCTGC	350
	AGCGAG	CTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT	400
	CAGCAG	SCAAG TTCCACGCCA AAGGCGACCA TGAGATTAAT GCAGAGGAGA	450
30	TGAAG	GGTGC CARAGARATG GCCGAGARAC TTTTRAGGGC GGTTGAGACC	500
	TACCT	ATTGG CACACTCTGC TGAATACAAC TAAATATCGT CTTGTGTCTT	550
	CGCCC	RATAA TAACTTGTAC GTGGCTTTCA TGTTTTTTTT TTAAAACTTT	
	GATTA	CTTGC TAATAAAGGA GCTTGCGGTT GTGTTCATCT GCTTGCTGAA	600 650
	ATCGA'	TGTTG TAACTCGGAA GAATGCAAAC TGAATGTTGT ATTACTTTTT	
3	GCATA	TATAC ARATANTGGA ARGGATANCA TCATTGANGT TCANANANANA	700
	AAAAA	AA AAAAAAAAA AAAAAAAA AAAAAAAAA AAAAA	742

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	(i)	SEQUENCE CHARACTERISTICS:	J.
		(A) LENGTH: 480 nucleotides	
5		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA of mRNA	
	(iii)	HYPOTHETICAL: no	
10	(iv)	ANTI-SENSE: no	
	(V)	FRAGMENT TYPE: not applicable	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: hazel (Corylus sp.)	
	(vii)	IMMEDIATE SOURCE:	
15		(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN	
	(viii)	POSITION IN GENOME: not applicable	
	(ix)	FEATURE: not applicable	
	(x)	PUBLICATION INFORMATION: not applicable	
20	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO: 13	
	ATGGGT	GTTT TCAATTACGA GGTTGAGACT CCCTCCGTTA TCCCAGCGGC	50
	AAGGCT	GTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG	100
	TTGCAC	CTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG	150
25	CCTGGA	ACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA	200
	CGTGAA	GGAG AGGGTTGATG AGGTTGACAA CACAAACTTC AAATATAGCT	250
	ACACCG'	TGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC	300
	AGCGAG	CTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT	350
	CAGCAG	CAAG TTCCACGCCA AAGGCGACCA TGAGATTAAT GCAGAGGAGA	400
30	TGAAGG	GTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC	450
	TACCTA:	TTGG CACACTCTGC TGAATACAAC	480

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
- 5 (B) TYPE: amino acid
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: not applicable
- 10 (V) FRAGMENT TYPE: not applicable
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: hazel (Corylus sp.)
 - (vii) IMMEDIATE SOURCE:
 - (A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
- 15 (viii) POSITION IN GENOME: not applicable
 - (ix) FEATURE: not applicable
 - (x) PUBLICATION INFORMATION: not applicable
 - (xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 14

- 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 Met Gly Val Phe Asn Tyr Glu Val Glu Thr Pro Ser Val Ile Pro
- 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 25 Ala Ala Arg Leu Phe Lys Ser Tyr Val Leu Asp Gly Asp Lys Leu
 - 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 Ile Pro Lys Val Ala Pro Gln Ala Ile Thr Ser Val Glu Asn Val
- 30 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 Glu Gly Asn Gly Gly Pro Gly Thr Ile Lys Asn Ile Thr Phe Gly
 - 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 Glu Gly Ser Arg Tyr Lys Tyr Val Lys Glu Arg Val Asp Glu Val
- 35 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 Asp Asn Thr Asn Phe Lys Tyr Ser Tyr Thr Val Ile Glu Gly Asp
- 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 40 Val Leu Gly Asp Lys Leu Glu Lys Val Cys Ser Glu Leu Lys Ile
 - 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 Val Ala Ala Pro Gly Gly Gly Ser Il Leu Lys Ile S r Ser Lys

121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 Phe His Ala Lys Gly Asp His Glu Ile Asn Ala Glu Glu Met Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 5 Gly Ala Lys Glu Met Ala Glu Lys Leu Leu Arg Ala Val Glu Thr

151 152 153 154 155 156 157 158 159 160 Tyr Leu Leu Ala His Ser Ala Glu Tyr Asn

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	(i)	SEQUENCE CHARACTERISTICS:	
	•	(A) LENGTH: 655 nucleotides	
5		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA of mRNA	
	(iii)	HYPOTHETICAL: no	
10		ANTI-SENSE: no	
	(V)	FRAGMENT TYPE: not applicable	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: hazel (Corylus sp.)	
	(vii)	IMMEDIATE SOURCE:	
15		(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN	
	(viii)	POSITION IN GENOME: not applicable	
	(ix)	FEATURE: not applicable	
	(x)	PUBLICATION INFORMATION: not applicable	
	•	1F	
20	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO: 15	
		GTTT TCAATTACGA GGCTGAGACC ACCTCCGTTA TCCCTGCGGC	50
	ATGGGT	GTTC AAGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG	100
		CTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG	150
25	COMOCA	ACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA	200
23	CCIGGN	GGAG AGGGTTGATG AGGTTGACAA CACAAACTTC ACATACAGCT	250
	ACACCG	TGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC	300
	CACGAG	CTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT	350
	CAGCAG	CARG TTCCACGCCA AAGGTGACCA TGAGATTAAT GCAGAGGAGA	400
30		GTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC	450
	TACCTA	ATTGG CACACTCTGC TGAATACAAC TAAACCTCGT CTTGTGTCTT	500
	CGCCCA	AATAA TAGCTTGTAC GTGGCTTTCA TGTTTTTTTT TTAAACTTTG	550
	TTTTCT	TTGCT AATAAAGGAG CTTGCGGTTG TGTTCATCTG CTTGCTGAAG	600
	ATCGAT	TGTTG TAACTCGGAA GAATGCAAAT TTAATGTTGT ATTAAAAAAA	650
			655

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	INFORM	ATION FOR SEQ ID NO: 16	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 480 nucleotides	
		(B) TYPE: nucleic acid	
5		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA of mRNA	
	(iii)	HYPOTHETICAL: no	
	(iv)	ANTI-SENSE: no	
10	(♥)	FRAGMENT TYPE: not applicable	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: hazel (Corylus sp.)	
	(vii)	IMMEDIATE SOURCE:	
		(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN	
15	(viii)	POSITION IN GENOME: not applicable	
	(ix)	FEATURE: not applicable	
	(x)	PUBLICATION INFORMATION: not applicable	
	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO: 16	
20			
	ATGGGT	GTTT TCAATTACGA GGCTGAGACC ACCTCCGTTA TCCCTGCGGC	50
	AAGGCT	GTTC ARGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG	100
	TTGCAC	CTCA AGCTATTACC AGCGTTGAAA ACGTTGAAGG AAATGGAGGG	150
	CCTGGA	ACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA	200
25	CGTGAA	GGAG AGGGTTGATG AGGTTGACAA CACAAACTTC ACATACAGCT	250
	ACACCG	TGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAGGTCTGC	300
	CACGAG	CTGA AGATAGTGGC AGCCCCTGGT GGAGGATCCA TCTTGAAGAT	350
	CAGCAG	CAAG TTCCACGCCA AAGGTGACCA TGAGATTAAT GCAGAGGAGA	400
	TGAAGG	GTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC	450
30	TACCTA	TTGG CACACTCTGC TGAATACAAC	480

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
- 5 (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: not applicable
 - (v) FRAGMENT TYPE: not applicable
- 10 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: hazel (Corylus sp.)
 - (vii) IMMEDIATE SOURCE:
 - (A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
 - (viii) POSITION IN GENOME: not applicable
- 15 (ix) FEATURE: not applicable
 - (x) PUBLICATION INFORMATION: not applicable
 - (xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 17
- 20 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 Met Gly Val Phe Asn Tyr Glu Ala Glu Thr Thr Ser Val Ile Pro
- 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 Ala Ala Arg Leu Phe Lys Ser Tyr Val Leu Asp Gly Asp Lys Leu
 25
 - 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45

 The Pro Lys Val Ala Pro Gln Ala The Thr Ser Val Glu Asn Val
- 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 30 Glu Gly Asn Gly Gly Pro Gly Thr Ile Lys Asn Ile Thr Phe Gly
 - 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 Glu Gly Ser Arg Tyr Lys Tyr Val Lys Glu Arg Val Asp Glu Val
- 35 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 Asp Asn Thr Asn Phe Thr Tyr Ser Tyr Thr Val Ile Glu Gly Asp
 - 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 Val Leu Gly Asp Lys Leu Glu Lys Val Cys His Glu Leu Lys Ile
- 40 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 Val Ala Ala Pr Gly Gly Gly Ser Ile Leu Lys Ile S r Ser Lys
 - 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135

Phe His Ala Lys Gly Asp His Glu Ile Asn Ala Glu Glu Met Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 Gly Ala Lys Glu Met Ala Glu Lys Leu Arg Ala Val Glu Thr

151 152 153 154 155 156 157 158 159 160 Tyr Leu Leu Ala His Ser Ala Glu Tyr Asn

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INFORMATION FOR SEQ ID NO: 18

	(i)	SEQUENCE CHARACTERISTICS:	
	\- ,	(A) LENGTH: 860 nucleotides	
5		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA of mRNA	
	(iii)	HYPOTHETICAL: no	
10	(iv)	ANTI-SENSE: no	
	(V)	FRAGMENT TYPE: not applicable	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: hazel (Corylus sp.)	
	(vii)	IMMEDIATE SOURCE:	
15		(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN	
	(viii)	POSITION IN GENOME: not applicable	
	(ix)	FEATURE: not applicable	
	(x)	PUBLICATION INFORMATION: not applicable	
			-
20	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO: 18	
		TOTAL COLORS BOROLOGICA	50
	ATGGGT	CETTT TCAATTACGA GGTTGAGACC CCCTCCGTTA TCTCAGCGGC	100
	AAGGCI	COTTO AAGTOCTATG TOOTTGATGG CGATAAGCTO ATCCCAAAGG	150
	TTGCAC	CTCA AGCTATTACC AGCGTTGAAA ACGTTGGAGG AAATGGAGGG	200
25	CCTGGI	ARCCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA	250
	CGTGA	AGGAG AGGGTTGATG AGGTTGACAA CACAAACTTC AAATATAGCT	300
	ACACCO	STGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAAGTCTGC	350
	AGCGAG	SCTGA AGATAGTGGC AGCCCCTGGT GGGGGATCCA CCTTGAAGAT	400
	CAGCA	SCAAG TTCCACGCCA AAGGTGACCA TGAGATTAAT GCAGAGGAGA	450
30	TGAAG	GGTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC	500
	TACCT	ATTGG CACACTCTGC TGAATACAAC TAAATATCGT CTTGTGTCTT	550
	CGCCA	ATAAT AACTTGTACG TGGCTTTCAT GTTTTTTTTT AAAAAACTTT	600
	GTTTA	CTTGC TAATAAAGGA GCTTGCGGTT GTGTTCATCT GCTTGCTGAA	650
	ATCGA'	TGTTG TAACTCGGAA GAATGCAAAC TGAATGTTGT ATTACTTTTT	700
35	GCATA	TATAC AAATAATGGA AAGGATAACA TCATTGAAGT TCAAAAAAAA	750
	GAAAA	AAAAA AGCTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTT	800
	ATTTT	AACCC GATACTGATA CTCAAAAATG CAAGAGAGTT TCCGCATAAG	850
	CACAA	TTTGT TTATGTTGAC TTAATACATT ATAAGCAAAA AAAAAAAAAA	

AAAAAAAAA

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INFORMATI N FOR SEQ ID NO: 19

	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 480 nucleotides	
5		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA of mRNA	
	(iii)	HYPOTHETICAL: no	
10	(iv)	ANTI-SENSE: no	
	(V)	FRAGMENT TYPE: not applicable	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: hazel (Corylus sp.)	
	(vii)	IMMEDIATE SOURCE:	
15		(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN	:
	(viii)	POSITION IN GENOME: not applicable	
	(ix)	FEATURE: not applicable	
	(x)	PUBLICATION INFORMATION: not applicable	
20	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO: 19	
		STTT TCAATTACGA GGTTGAGACC CCCTCCGTTA TCTCAGCGGC	50
		STTC ARGTCCTATG TCCTTGATGG CGATAAGCTC ATCCCAAAGG	100
		CTCA AGCTATTACC AGCGTTGAAA ACGTTGGAGG AAATGGAGGG	150
25		ACCA TCAAGAATAT CACCTTTGGC GAAGGCAGCC GTTACAAGTA	200
		GGAG AGGGTTGATG AGGTTGACAA CACAAACTTC AAATATAGCT	250
		TGAT CGAGGGTGAT GTCCTGGGTG ACAAGCTGGA GAAAGTCTGC	300
	AGCGAG	CTGA AGATAGTGGC AGCCCCTGGT GGGGGATCCA CCTTGAAGAT	350

CAGCAGCAAG TTCCACGCCA AAGGTGACCA TGAGATTAAT GCAGAGGAGA

30 TGAAGGGTGC CAAAGAAATG GCCGAGAAAC TTTTAAGGGC GGTTGAGACC

TACCTATTGG CACACTCTGC TGAATACAAC

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INFORMATION FOR SEQ ID NO: 20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
- 5 (B) TYPE: amino acid
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: not applicable
- 10 (v) FRAGMENT TYPE: not applicable
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: hazel (Corylus sp.)
 - (vii) IMMEDIATE SOURCE:
 - (A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
- 15 (viii) POSITION IN GENOME: not applicable
 - (ix) FEATURE: not applicable
 - (x) PUBLICATION INFORMATION: not applicable
 - (xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 20

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- 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 Met Gly Val Phe Asn Tyr Glu Val Glu Thr Pro Ser Val Ile Ser
- 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 25 Ala Ala Arg Leu Phe Lys Ser Tyr Val Leu Asp Gly Asp Lys Leu
 - 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 Ile Pro Lys Val Ala Pro Gln Ala Ile Thr Ser Val Glu Asn Val
 - 30 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 Gly Gly Asn Gly Gly Pro Gly Thr Ile Lys Asn Ile Thr Phe Gly
 - 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 Glu Gly Ser Arg Tyr Lys Tyr Val Lys Glu Arg Val Asp Glu Val
 - 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 Asp Asn Thr Asn Phe Lys Tyr Ser Tyr Thr Val Ile Glu Gly Asp
 - 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 40 Val Leu Gly Asp Lys Leu Glu Lys Val Cys Ser Glu Leu Lys Ile
 - 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 Val Ala Ala Pro Gly Gly Gly Ser Thr Leu Lys Ile Ser Ser Lys

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121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 Phe His Ala Lys Gly Asp His Glu Ile Asn Ala Glu Glu Met Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 5 Gly Ala Lys Glu Met Ala Glu Lys Leu Leu Arg Ala Val Glu Thr

151 152 153 154 155 156 157 158 159 160 Tyr Leu Leu Ala His Ser Ala Glu Tyr Asn

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INFORMATION FOR SEQ ID NO: 21

	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 672 nucleotides	
5		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA of mRNA	
	(iii)	HYPOTHETICAL: no	
LO.	(iv)	ANTI-SENSE: no	
	(V)	FRAGMENT TYPE: not applicable	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: birch (Betula sp.)	
	(vii)	IMMEDIATE SOURCE:	
L5		(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN	
	(viii)	POSITION IN GENOME: not applicable	
		FEATURE: not applicable	
	(x)	PUBLICATION INFORMATION: not applicable	
20	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO: 21	
		•	
		GTTT TCAATTACGA AACTGAGACC ACCTCTGTTA TCCCAGCAGC	50
		GTTC AAGGCCTTTA TCCTTGATGG CGATAATCTC TTTCCAAAGG	100
		CCCA AGCCATTAGC AGTGTTGAAA ACATTGAAGG AAATGGAGGG	150
25		ACCA TTAAGAAGAT CAGCTTTCCC GAAGGCTTCC CTTTCAAGTA	200
		GGAC AGAGTTGATG AGGTGGACCA CACAAACTTC AAATACAATT	250
		TGAT CGAGGGCGGT CCCATAGGCG ACACATTGGA GAAGATCTCC	300
		ATAA AGATAGTGGC AACCCCTGAT GGAGGATCCA TCTTGAAGAT	350
		CARG TACCACACCA AAGGTGACCA TGAGGTGAAG GCAGAGCAGG	400
30		CARG TARAGARATG GGCGAGACAC TTTTGAGGGC CGTTGAGAGC	450
		TTGG CACACTCCGA TGCCTACAAC TAATTAATTA ACTTGTGTCG	500
•		ACAT GTCCCTGATC AATAATGGGT TGCAGTGTTC ATGGTGTTTT	550
		CTAR TARAGGAGCT TGCAGTTGTG ATCATCTGCT TGCTAGCTGA	600
	AGATGT	TGTA ATTTATTGGG AGAATGATAA TAAATGTTCT ATTAAAAAAA	650
2 5		AAAAAAAAA AA	672

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	INFORM	ATION FOR SEQ ID NO: 22	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 480 nucleotides	
		(B) TYPE: nucleic acid	
5		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA of mRNA	
	(iii)	HYPOTHETICAL: no	
	(iv)	ANTI-SENSE: no	
10	(V)	FRAGMENT TYPE: not applicable	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: birch (Betula sp.)	
	(vii)	IMMEDIATE SOURCE:	
		(A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN	
15	(viii)	POSITION IN GENOME: not applicable	
	(ix)	FEATURE: not applicable	
	(x)	PUBLICATION INFORMATION: not applicable	
	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO: 22	
20	•	-	
	ATGGGT	GTTT TCAATTACGA AACTGAGACC ACCTCTGTTA TCCCAGCAGC	50
	TCGACTO	GTTC AAGGCCTTTA TCCTTGATGG CGATAATCTC TTTCCAAAGG	100
	TTGCAC	CCCA AGCCATTAGC AGTGTTGAAA ACATTGAAGG AAATGGAGGG	150
25	CCTGGAI	ACCA TTAAGAAGAT CAGCTTTCCC GAAGGCTTCC CTTTCAAGTA	200
	CGTGAAG	GGAC AGAGTTGATG AGGTGGACCA CACAAACTTC AAATACAATT	250
	ACAGCG:	TGAT CGAGGGCGGT CCCATAGGCG ACACATTGGA GAAGATCTCC	300
	AACGAGA	ATAA AGATAGTGGC AACCCCTGAT GGAGGATCCA TCTTGAAGAT	350

CAGCAACAAG TACCACCA AAGGTGACCA TGAGGTGAAG GCAGAGCAGG

30 TTAAGGCAAG TAAAGAAATG GGCGAGACAC TTTTGAGGGC CGTTGAGAGC

TACCTCTTGG CACACTCCGA TGCCTACAAC

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INFORMATION FOR SEQ ID NO: 23

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
- 5 (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: not applicable
 - (v) FRAGMENT TYPE: not applicable
- 10 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: birch (Betula sp.)
 - (vii) IMMEDIATE SOURCE:
 - (A) POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
 - (viii) POSITION IN GENOME: not applicable
- 15 (ix) FEATURE: not applicable
 - (x) PUBLICATION INFORMATION: not applicable
 - (xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 23
- 20 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 Met Gly Val Phe Asn Tyr Glu Thr Glu Thr Thr Ser Val Ile Pro
 - 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 Ala Ala Arg Leu Phe Lys Ala Phe Ile Leu Asp Gly Asp Asn Leu
 - 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 Phe Pro Lys Val Ala Pro Gln Ala Ile Ser Ser Val Glu Asn Ile
- 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 30 Glu Gly Asn Gly Gly Pro Gly Thr Ile Lys Lys Ile Ser Phe Pro
 - 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 Glu Gly Phe Pro Phe Lys Tyr Val Lys Asp Arg Val Asp Glu Val
- 35 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 Asp His Thr Asn Phe Lys Tyr Asn Tyr Ser Val Ile Glu Gly Gly
 - 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 Pro Ile Gly Asp Thr Leu Glu Lys Ile Ser Asn Glu Ile Lys Ile
- 40 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 Val Ala Thr Pro Asp Gly Gly Ser Ile Leu Lys Ile S r Asn Lys
 - 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135

Tyr His Thr Lys Gly Asp His Glu Val Lys Ala Glu Gln Val Lys

136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 Ala Ser Lys Glu Met Gly Glu Thr Leu Leu Arg Ala Val Glu Ser

151 152 153 154 155 156 157 158 159 160 Tyr Leu Leu Ala His Ser Asp Ala Tyr Asn

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CLAIMS

- A recombinant DNA molecule, comprising a DNA coding for a polypeptide having at least one epitope of an allergen of trees of the order Fagales, the allergen is
 Selected from the group Aln g I, Cor a I or Bet v I.
 - 2. A recombinant DNA molecule according to claim 1, wherein the allergen Aln g I. Cor a I or Bet v I is selected from the group consisting of birch, alder, hazel and hornbeam.
- 3. A recombinant DNA molecule according to claim 1, wherein the epitopes of 10 the allergens having an amino acid sequence selected from the following group

GlyValPheAsnTyrGlu

PhelleLeuAspGlyAspLysLeu

AlaIleSerSerValGluAsnIle

Gly Asn Gly Gly ProGly Thr I le Lys Lys Lie Ser Phe

- 15 LysTyrVaiLysAspArgValAspGluValAsp
 - LeuLeuArgAlaValGluSerTyrLeuLeuAlaHisSer
 - 4. A recombinant DNA molecule according to claim 1 having at least 60% identity to the nucleotid sequence as shown in SEQ ID No. 2.
- 5. A recombinant DNA molecule according to claim 1, wherein the allergen is 20 an Aln g I allergen of alder.
 - 6. A recombinant DNA molecule according to claim 1, 2, 3, 4 or 5 which codes for a polypeptide having the entire amino acid sequence of an Aln g I allergen.
- 7. A recombinant DNA molecule according to claim 5, which codes for a polypeptide having all or part of the amino acid sequence as defined in the Sequence 25 Listing by SEQ ID NO:3.
 - 8. A recombinant DNA molecule according to claim 1, wherein the allergen is a Cor a I allergen of hazel.
 - 9. A recombinant DNA molecule according to claim 1 or 8, which codes for a polypeptide having the entire amino acid sequence of a <u>Cor a I</u> allergen.

- 10. A recombinant DNA molecule according to claim 1 having at least 60% identity to the nucleotid sequence as shown in SEQ ID NOs. 10, 13, 16, and 19.
- 11. A recombinant DNA molecule according to claim 8 which codes for a polypeptide having all or part of the amino acid sequence as defined in the Sequence Li-5 sting by SEQ ID NOs. 11, 14, 17, and 20.
- 12. A recombinant DNA molecule according to claim 1 wherein the allergen is a <u>Bet v I</u> allergen of birch.
- 13. A recombinant DNA molecule according to claim 1 having at least 60% identity to the nucleotid sequence as shown in SEQ ID No. 22.
- 10 14. A recombinant DNA molecule according to claim 12, which codes for a polypeptide having all or part of the amino acid sequence as defined in the Sequence Listing by SEQ ID NO. 23.
 - 15. A recombinant DNA molecule according to claim 3 which codes for one of the epitopes of the allergens as listed in claim 3.
- 16. A polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen showing the same or a similar capacity to bind IgE from tree pollen allergic individual's sera.
- 17. A replicable prokaryotic or eukaryotic expression vehicle capable, in a transformant prokaryotic or eukaryotic host organism, of being replicated and of 20 directing expression of a DNA of claim 1 to 15 to produce said polypeptides.
 - 18. A prokaryotic or eukaryotic host organism transformed with an expression vehicle capable, in said host organism, of being replicated and of directing expression of a DNA of claim 1 to 15 to produce said polypeptides.
- 19. A host organism according to claim 18, wherein the organism is <u>Escheri-</u>25 chia coli.
- 20. A method for producing a polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen, comprising culturing a prokaryotic or eukaryotic host organism containing an expression vehicle capable, in said host organism, of being replicated and of directing expression of a DNA of claim 1 to 15 to produce 30 said polypeptides.

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- 21. A composition comprising a polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen and produced by a method according to claim 20.
- 22. A composition comprising a polypeptide having at least one epitope of an Aln g I allergen and produced by a chemical synthesis according to amino acid sequence as defined in the Sequence Listing by SEQ ID NO. 3.
- 23. A composition comprising a polypeptide having at least one epitope of a Cor a I allergen and produced by a chemical synthesis according to amino acid se-10 quence as defined in the Sequence Listing SEQ ID NOs.11, 14, 17 and 20.
 - 24. A composition comprising a polypeptide having at least one epitope of a <u>Bet</u> v I allergen and produced by chemical synthesis according to the amino acid sequence as defined in the Sequence Listing by SEQ ID No. 23.
- 25. An isolated allergenic peptide of pollen of trees of the order Fagales, ha-15 ving at least one of the epitopes with amino acid sequence listed in claim 3.
 - 26. A peptide according to claim 6, 7, 8, 9, 11, 12, 14, or 25, capable of modifying in a sensitive individual to whom it is administered, an allergic response to a pollen of a tree of the order Fagales.
- 27. A peptide according to claim 26 capable of modifying T-cell response to a 20 pollen of trees of the order Fagales.
 - 28. An isolated peptide of the claim 6, 7, 8, 9, 11, 12, 14 or 25 capable of interfering with an allergic response.
- 29. A method for detecting IgE antibodies comprising contacting serum of a mammal with a composition according to claim 21, and detecting any immunological 25 reaction between IgE antibodies in the serum and said polypeptide having at least one epitope of an Aln g I, a Cor a I or a Bet v I allergen.
 - 30. A method for detecting allergic reactions to an Aln g I, a Cor a I or a Bet v I allergen, comprising challenging a mammal with a composition according to claim 21 so as to elicit bronchial, conjunctival, dermal, nasal or oral provocation of said

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mammal, and detecting any immunological reaction between said tissues and said polypeptides.

- 31. A method for detecting in vitro a cellular reaction to an Aln g I, a Cor a I or a Bet v I allergen, comprising contacting mammalian cells with a composition 5 according to claim 21, and detecting any reaction between said cells and said polypeptide.
 - 32. A method for treating a mammal afflicted with a pollen allergy, comprising administering an effective amount of a composition according to claim 21 to hyposensitize said mammal to an Aln g I, a Cor a I or a Bet v I allergen.

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AAG Lys CCC Pro Trc Phe TGT Cys AGC Ser AAG Lys AAC Asn AAC Asn TAC Tyr CTG Leu GTT Val TTT Phe GTC Val CGG Arg ACC Thr GTA Val AAG Lys AGC Ser AAA Lys GCC Ala GCT Ala GCT Ala CGC Arg ATC Ile GAA Glu ATC Ile GAG Glu AAG Lys AAG Lys GCG Ala GAT Asp CTG Leu ATT Ile TCT Ser CCT Pro CCA Pro AAG Lys GCA Ala TTG Leu GCA Ala AAG Lys GTT Val ATC Ile ATC Ile ATC Ile GAC Asp GCA Ala GTT Val GAG Glu ACC Thr GGC G1y Grr Val AAG Lys TCC Ser GAT Asp TTG Leu GGA G1y TCC Ser GGA G1y CCA Pro GTT Val GTG Val CCC Pro AGG Arg GCC Ala GGA G1y CTT Leu CCT Pro GCA Ala TAC TYT ACC Thr GAT ASP 666 61y **GA**G Glu GGT Gly AGC Ser CTC Leu gaa Glu AAG Lys GGA G1y AAG Lys GGT Gly CCT Pro ATA Ile GAG Glu GCC Ala GAT ASP AAT Asn GTA Val GAA Glu 66C 61y GGA Gly TAC TYF ATC Ile GCA Ala CAT His GCC Ala TAC GAT ASP GAA Glu AAG Lys GTG Val GTG Val GAC ASP AAG Lys TTT Phe S AAT Asn ATA Ile GGC Gly CIT ATT Ile AGC Ser TTC Phe CCT Pro AAC Asn TTC Phe ATC Ile AAG Lys AAA Lys CTT Leu Grr Val TTT Phe GAG Glu AGC Ser AGC Ser ATC Ile ACC Thr GGA G1y GGC G1y GAG Glu CAC His GTG Val GGT Gly GCC Ala GTT Val TAC TYF GCC Ala AAG Lys GAA G1u AAA Lys AAC Asn TTC Phe AGT Ser

attictgcctaatttttgatcagcttgcatgtgttcttgtcaagccataaatactgcttaacttcgtcttgct<u>aata</u>

<u>aa</u>tgaagctgttgtagtcgtttatgagtacgtaataatgacaccaaacatatggagccaattgcttatgaatagaagtt Aagttcttaaaaaaaaaaaaaaaaa

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FIGURE 2

 1
 11
 21
 31
 41

 5'-TTTAATACGA CTCACTATAG ATCTCCCGGG AAGCTTTTTT TTTTTTTTT-3'
 T7 Primer
 Bg1II
 HindIII

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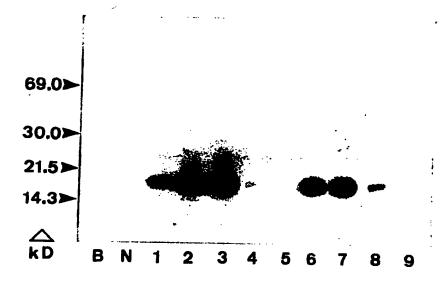


Fig. 3



Fig. 4

69.0➤

30.0➤

21.5➤

14.3➤

A B N 1 2 3 4 5 6 7 8 9

Fig. 5

69.0>

30.0➤

21.5➤

14.3>

Fig. 6

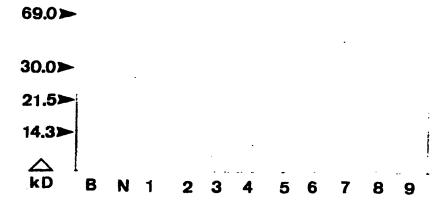


Fig. 7

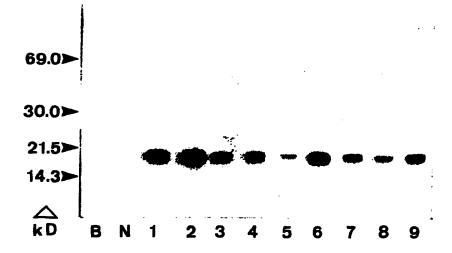


Fig. 8

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69.0➤
30.0➤
21.5➤
14.3➤

B N 1 2 3 4 5 6 7 8 9

Fig. 9

69.0 > 30.0 > 21.5 > 14.3 > B N 1 2 3 4 5 6 7 8 9

Fig. 10

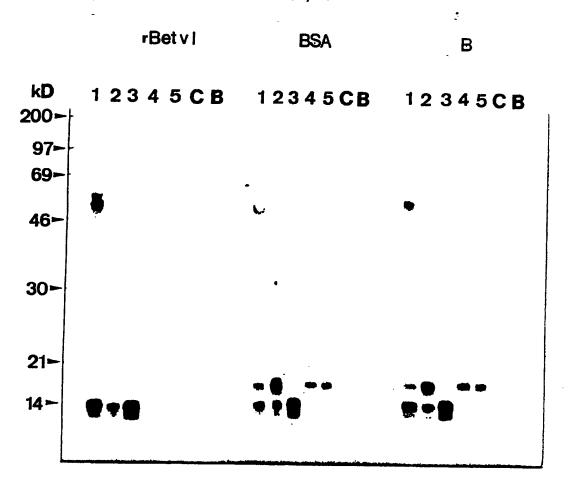


FIG. 11